

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 17, 2006, 09:42:00 ; Search time 25.6 Seconds

(without alignments)
96.114 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTAACACAGACTTCATTGTC 28

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A.Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	251	2	AAR63923 Type I RI
2	45	84.9	132	3	AAG59355 Arabidops
3	45	84.9	190	3	AAG59354 Arabidops
4	45	84.9	196	3	AAG60327 Arabidops
5	45	84.9	220	3	AAG59642 Arabidops
6	45	84.9	257	3	AAG60333 Arabidops
7	45	84.9	263	3	AAG60326 Arabidops
8	45	84.9	286	3	AAG04861 Arabidops
9	45	84.9	287	3	AAG59641 Arabidops

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c	11	45	84.9	321	3	AAG60325 Arabidops
c	12	45	84.9	327	3	AAG60331 Arabidops
c	13	45	84.9	344	3	AAG04860 Arabidops
c	14	45	84.9	345	3	AAG59640 Arabidops
c	15	45	84.9	356	3	AAG04859 Arabidops
c	16	43	81.1	235	2	AAR63913 Type I RI
c	17	43	81.1	251	2	AAR63791 plant typ
c	18	43	81.1	251	2	AAR63903 Type I RI
c	19	43	81.1	251	2	AAR63914 Type I RI
c	20	43	81.1	251	2	AAR63922 Type I RI
c	21	43	81.1	251	2	AAR63916 Type I RI
c	22	43	81.1	251	2	AAR63921 Type I RI
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c	24	43	81.1	251	2	AAR63918 Type I RI
c	25	43	81.1	251	2	AAR63920 Type I RI
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c	27	43	81.1	251	2	AAR63919 Type I RI
c	28	43	81.1	251	2	AAR63924 Type I RI
c	29	43	81.1	251	2	AAR63912 Type I RI
c	30	43	81.1	251	2	AAR74177 Type I RI
c	31	43	81.1	251	8	ADG63044 Gelonium
c	32	43	81.1	293	2	AAW29300 BPI pepti
c	33	43	81.1	309	2	AAW29303 BPI pepti
c	34	43	81.1	316	5	ABG71551 G. multif
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c	36	43	81.1	498	9	AEB68722 scFv23-ge
c	37	43	81.1	507	5	ABG71552 Murine sc
c	38	39	73.6	123	4	AAG73777 Human col
c	39	39	73.6	161	5	ABP64462 Human ORF
c	40	39	73.6	208	6	ABO00814 Polypepti
c	41	39	73.6	258	2	AAR22227 Gelonin t
c	42	39	73.6	284	6	ABO00515 Novel hum
c	43	39	73.6	288	8	ADR14645 Human NF-
c	44	39	73.6	303	4	AAG81254 Human AFP
c	45	39	73.6	311	5	AAO19377 Human pal

ALIGNMENTS

RESULT 1

AAR63923

ID AAR63923 standard; protein; 251 AA.

AC AAR63923;

XX 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

DE Type I RIP gelonin analog Gel (C103).

XX Type I ribosome-inactivating proteins; RIPS; gelonin;
XX cytotoxic therapeutic agents; autoimmune disease; cancer;
XX graft-versus-host disease.

OS Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GM;

XX WPI; 1995-006804/01.

PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.

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XX Example 3; Page 187-188; 22lpp; English.
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targetted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX SQ Sequence 251 AA;

Alignment Scores:
Pred. No.: 0.205 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

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QY 2 ACATGTAACAAGACTTCATTTCGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 2
AAGS9355
ID AAGS9355 standard; protein; 132 AA.
XX AAGS9355;
XX XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76769.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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Db 23 LysMetLysAlaCysPheThrCys 30
RESULT 3
AAGS9354
ID AAGS9354 standard; protein; 190 AA.
AC AAGS9354;
XX
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76768.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
PN EP1033405-A2.
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US-10-717-243-59 (1-28) x AAG59354 (1-190)

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RESULT 4

AAG60327

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XX AC AAG60327;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 78128.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX OS Arabidopsis thaliana.

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XX PD 06-SEP-2000.

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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Alignment Scores:

Pred. No.: 7.51 Length: 263
Score: 45.00 Matches: 7
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 87.5% Mismatches: 0
Query Match: 84.9% Indels: 0
DB: 3 Gaps: 0

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Db 148 LysMetLysAlaCysPheThrCys 155

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AC AAG04861;

XX DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 1048.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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Alignment Scores:
Pred. No.: 7.55
Score: 45.00
Percent Similarity: 100.0%

Length: 321
Matches: 7
Conservative: 1

Best Local Similarity: 87.5% Mismatches: 0
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DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x AAG60325 (1-321)

QY 25 AAAATGAAGTCTGTTTACATGT 2

DB 206 LysMetLysAlaCysPheThrCys 213

RESULT 12

AAG60331

ID AAG60331 standard; protein; 327 AA.

XX

AC AAG60331;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 78134.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

XX 25-FEB-2000; 2000EP-00301439.

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Percent Similarity:	100.0%	
Best Local Similarity:	87.5%	1
Query Match:	84.9%	0
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Conservative:		1
Mismatches:		0
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XX	DT 17-OCT-2000 (first entry)		
XX	DE Arabidopsis thaliana protein fragment SEQ ID NO: 1047.		
XX	KW Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX	OS Arabidopsis thaliana.		
XX	PN EP1033405-A2.		
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Alignment Scores:

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Length: 344
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Conservative: 1
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US-10-717-243-59 (1-28) x AAG04860 (1-344)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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Best Local Similarity:	87.5%	Mismatches:	0
Query Match:	84.9%	Indels:	0
DB:	3	Gaps:	0

US-10-717-243-59 (1-28) x AAG04859 (1-356)

Oy 25 AAAATGAAGTCTTGTGTTTATCATGT 2
|||||:|||||

Db 218 LysMetLysAlaCysPheThrCys 225

Search completed: February 17, 2006, 09:46:27
Job time : 130 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 17, 2006, 09:51:45 ; Search time 6.6 seconds
(without alignments)
70.149 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTAAACACAGCTTCATTTGGC 28

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Fgapop 10.0, Fgapext 0.5

Dgapop 6.0, Dgapext 7.0

Delopt 6.0, Delopt 7.0

Searched: 572060 seqs; 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSWEB/spool/US10717243/runat_16022006_160654_2293/app_query.fasta_1
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs02p -USER=US10717243@CGN_1_1_71@runat_16022006_160654_2293 -NCPUs=6
-ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pcp:*

2: /cgn2_6/prodata/1/iaa/6 COMB.pcp:*

3: /cgn2_6/prodata/1/iaa/H COMB.pcp:*

4: /cgn2_6/prodata/1/iaa/H COMB.pcp:*

5: /cgn2_6/prodata/1/iaa/RE COMB.pcp:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	251	1	US-08-425-336-108
2	53	100.0	251	1	US-08-488-113B-108
3	53	100.0	251	1	US-08-477-484B-108
4	53	100.0	251	1	US-08-646-360-108
5	53	100.0	251	2	US-08-839-765-108
6	53	100.0	251	2	US-09-136-389-108
7	53	100.0	251	2	US-09-610-838-108
8	53	100.0	251	2	US-09-711-485-108
9	43	81.1	251	1	US-07-901-707-2
10	43	81.1	251	1	US-07-988-430-2
11	43	81.1	251	1	US-08-425-336-2
12	43	81.1	251	1	US-08-425-336-99

13	43	81.1	251	1	US-08-425-336-100	Sequence 100, App
14	43	81.1	251	1	US-08-425-336-101	Sequence 101, App
15	43	81.1	251	1	US-08-425-336-102	Sequence 102, App
16	43	81.1	251	1	US-08-425-336-103	Sequence 103, App
17	43	81.1	251	1	US-08-425-336-104	Sequence 104, App
18	43	81.1	251	1	US-08-425-336-105	Sequence 105, App
19	43	81.1	251	1	US-08-425-336-106	Sequence 106, App
20	43	81.1	251	1	US-08-425-336-107	Sequence 107, App
21	43	81.1	251	1	US-08-425-336-109	Sequence 109, App
22	43	81.1	251	1	US-08-425-336-110	Sequence 110, App
23	43	81.1	251	1	US-08-425-336-111	Sequence 111, App
24	43	81.1	251	1	US-08-488-113B-2	Sequence 2, Appl
25	43	81.1	251	1	US-08-488-113B-99	Sequence 99, Appl
26	43	81.1	251	1	US-08-488-113B-100	Sequence 100, App
27	43	81.1	251	1	US-08-488-113B-101	Sequence 101, App
28	43	81.1	251	1	US-08-488-113B-102	Sequence 102, App
29	43	81.1	251	1	US-08-488-113B-103	Sequence 103, App
30	43	81.1	251	1	US-08-488-113B-104	Sequence 104, App
31	43	81.1	251	1	US-08-488-113B-105	Sequence 105, App
32	43	81.1	251	1	US-08-488-113B-106	Sequence 106, App
33	43	81.1	251	1	US-08-488-113B-107	Sequence 107, App
34	43	81.1	251	1	US-08-488-113B-109	Sequence 109, App
35	43	81.1	251	1	US-08-488-113B-110	Sequence 110, App
36	43	81.1	251	1	US-08-488-113B-111	Sequence 111, App
37	43	81.1	251	1	US-08-477-484B-2	Sequence 2, Appl
38	43	81.1	251	1	US-08-477-484B-99	Sequence 99, Appl
39	43	81.1	251	1	US-08-477-484B-100	Sequence 100, App
40	43	81.1	251	1	US-08-477-484B-101	Sequence 101, App
41	43	81.1	251	1	US-08-477-484B-102	Sequence 102, App
42	43	81.1	251	1	US-08-477-484B-103	Sequence 103, App
43	43	81.1	251	1	US-08-477-484B-104	Sequence 104, App
44	43	81.1	251	1	US-08-477-484B-105	Sequence 105, App
45	43	81.1	251	1	US-08-477-484B-106	Sequence 106, App

ALIGNMENTS

RESULT 1

US-08-425-336-108

; Sequence 108, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,336

; FILING DATE: 18-APR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

;
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-108 (1-251)

Qy 2 ACATGTAACACAGACTTCATTGGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 2

US-08-488-113B-108
; Sequence 108, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.

;
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-488-113B-108 (1-251)

Qy 2 ACATGTAACACAGACTTCATTGGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 3

US-08-477-484B-108
; Sequence 108, Application US/08477484B
; Patent No. 5756899
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-477-484B-108 (1-251)
QY 2 ACATGTAACAAAGACTTCATTTGCG 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 4
US-08-646-360-108
Sequence 108, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-646-360-108 (1-251)
QY 2 ACATGTAACAAAGACTTCATTTGCG 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 5
US-08-839-765-108
Sequence 108, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-839-765-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x US-08-839-765-108 (1-251)
QY 2 ACATGTAACAAACAGACTTCATTTGGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 6
US-09-136-389-108
/ Sequence 108, Application US/09136389
/ Patent No. 6146850
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-136-389-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x US-09-136-389-108 (1-251)
QY 2 ACATGTAACAAACAGACTTCATTTGGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 7
US-09-610-838-108
/ Sequence 108, Application US/09610838
/ Patent No. 6376217
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/610,838
/ FILING DATE: 06-JUL-2000
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/136,389
/ FILING DATE: 18-AUG-1998
/ APPLICATION NUMBER: 08/646,360
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
```

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-108

Alignment Scores: 251
Pred. No.: 9
Score: 53.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Matches: 9
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-717-243-59 (1-28) x US-09-610-838-108 (1-251)

QY 2 ACATGTAAACAAGACTTCATTGGC 28
DB 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 8

US-09-711-485-108
Sequence 108, Application US/09711485
Patent No. 6649742

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 110222US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-108

Alignment Scores: 251
Pred. No.: 9
Score: 53.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Matches: 9
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-717-243-59 (1-28) x US-09-711-485-108 (1-251)

QY 2 ACATGTAAACAAGACTTCATTGGC 28
DB 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 9

US-07-901-707-2
Sequence 2, Application US/07901707
Patent No. 5376546

GENERAL INFORMATION:
APPLICANT: Bernhardt, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.

TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707

FILING DATE: 19920619
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-901-707-2
Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-07-901-707-2 (1-251)
Qy 2 ACATGTAACAAAGACTTCATTTGGC 28
Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 10
US-07-988-430-2
; Sequence 2, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-988-430-2
Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-717-243-59 (1-28) x US-07-988-430-2 (1-251)
Qy 2 ACATGTAACAAAGACTTCATTTGGC 28
Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 11
US-08-425-336-2
; Sequence 2, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-2
Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0
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QY 2 ACATGTAAACAAGACTTCATTTGGC 28
Db 102 ThrilleysThraGleuHisPheGly 110

RESULT 12
US-08-425-336-99
; Sequence 99, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-99

Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-99 (1-251)
QY 2 ACATGTAAACAAGACTTCATTTGGC 28
Db 102 ThrilleysThraGleuHisPheGly 110

RESULT 13
US-08-425-336-100
; Sequence 100, Application US/08425336
; Patent No. 5621083

; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-100

Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-100 (1-251)
QY 2 ACATGTAAACAAGACTTCATTTGGC 28
Db 102 ThrilleysThraGleuHisPheGly 110

RESULT 14
US-08-425-336-101
; Sequence 101, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-101

Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-101 (1-251)
Oy 2 ACATGTAACAAGACTTCATTGGC 28
Db 102 ThrileysThrgLeuHisPheGly 110

RESULT 15
US-08-425-336-102
; Sequence 102 Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-102

Alignment Scores:
Pred. No.: 1.54 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-102 (1-251)
Oy 2 ACATGTAACAAGACTTCATTGGC 28
Db 102 ThrileysThrgLeuHisPheGly 110

Search completed: February 17, 2006, 09:53:33
Job time : 34 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 17, 2006, 10:07:00 : Search time 21.7 Seconds
(without alignments)
107.827 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTAACACAGACTTCATTGTC 28

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

Published Applications AA Main:
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	53	100.0	251	4	US-10-717-243-108
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4	43	81.1	251	4	US-10-127-890-2
5	43	81.1	251	4	US-10-127-890-99
6	43	81.1	251	4	US-10-127-890-100
7	43	81.1	251	4	US-10-127-890-101
8	43	81.1	251	4	US-10-127-890-102
9	43	81.1	251	4	US-10-127-890-103
10	43	81.1	251	4	US-10-127-890-104
11	43	81.1	251	4	US-10-127-890-105

12	43	81.1	251	4	US-10-127-890-106
13	43	81.1	251	4	US-10-127-890-107
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15	43	81.1	251	4	US-10-127-890-110
16	43	81.1	251	4	US-10-127-890-111
17	43	81.1	251	5	US-10-717-243-2
18	43	81.1	251	5	US-10-717-243-99
19	43	81.1	251	5	US-10-717-243-100
20	43	81.1	251	5	US-10-717-243-101
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29	43	81.1	251	5	US-10-717-243-111
30	43	81.1	293	3	US-09-765-527-259
31	43	81.1	309	3	US-09-765-527-253
32	43	81.1	316	4	US-10-074-596-1
33	43	81.1	332	3	US-09-765-527-251
34	43	81.1	498	5	US-10-964-195-13
35	43	81.1	507	4	US-10-074-596-11
36	43	81.1	751	6	US-11-084-080-26
37	41	77.4	42	4	US-10-425-115-186810
38	40	75.5	240	4	US-10-437-963-128893
39	39	73.6	123	4	US-10-106-698-4551
40	39	73.6	153	4	US-10-002-631C-44
41	39	73.6	161	3	US-09-867-550-1664
42	39	73.6	208	4	US-10-243-552-939
43	39	73.6	284	4	US-10-243-552-528
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45	39	73.6	317	4	US-10-106-698-5553

ALIGNMENTS

RESULT 1

US-10-127-890-108

; Sequence 108, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108

Alignment Scores:
Pred. No.: 0.22 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-108 (1-251)

Qy 2 ACATGTAACAAAGACTTCATTGGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 2

US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen P.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108

Alignment Scores:
Pred. No.: 0.22 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-717-243-59 (1-28) x US-10-717-243-108 (1-251)

Qy 2 ACATGTAACAAAGACTTCATTGGC 28
Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 3

US-09-765-527-247
; Sequence 247, Application US/09765527
; Patent No. US20020006838A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Alignment Scores:
Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x US-09-765-527-247 (1-251)

QY 2 ACATGTAACAAGACTTCATTGGC 28
DB 102 ThrileYsThrArgLeuHisPheGly 110

RESULT 4

US-10-127-890-2
; Sequence 2, Application US/10127890
; Publication NO. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2

Alignment Scores:
Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 4 Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-2 (1-251)

QY 2 ACATGTAACAAGACTTCATTGGC 28
DB 102 ThrileYsThrArgLeuHisPheGly 110

RESULT 5

US-10-127-890-99
; Sequence 99, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99

Alignment Scores: 18.5 Length: 251
Pred. No.: 43.00 Matches: 8
Score: 88.9% Conservative: 0
Percent Similarity: 88.9% Mismatches: 1
Best Local Similarity: 88.9% Indels: 0
Query Match: 81.1% Gaps: 0
DB: 4

US-10-717-243-59 (1-28) x US-10-127-890-99 (1-251)
Qy 2 ACATGTAACACAGACTTCATTTGGC 28
Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 6
US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100

Alignment Scores:
Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8

Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 4 Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-100 (1-251)
Qy 2 ACATGTAACACAGACTTCATTTGGC 28
Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 7
US-10-127-890-101
; Sequence 101, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-127-890-101

Alignment Scores:
Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8

US-10-717-243-59 (1-28) x US-10-127-890-

2 ACATGTAAACCAAGACTTCATTTC

Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 12

US-10-127-890-106
; Sequence 106, Application US/10127890
; Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 106:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 106:

US-10-127-890-106

Alignment Scores:

Pred. No.:	18.5	Length:	251
Score:	43.00	Matches:	8
Percent Similarity:	88.9%	Conservative:	0
Best Local Similarity:	88.9%	Mismatches:	1
Query Match:	81.1%	Indels:	0
DB:	4	Gaps:	0

US-10-717-243-59 (1-28) x US-10-127-890-106 (1-251)

Qy 2 ACATGTAACAAAGACTTCATTTCGC 28

Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 13

US-10-127-890-107
; Sequence 107, Application US/10127890
; Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 107:

US-10-127-890-107

Alignment Scores:

Pred. No.:	18.5	Length:	251
Score:	43.00	Matches:	8
Percent Similarity:	88.9%	Conservative:	0
Best Local Similarity:	88.9%	Mismatches:	1
Query Match:	81.1%	Indels:	0
DB:	4	Gaps:	0

US-10-717-243-59 (1-28) x US-10-127-890-107 (1-251)

Qy 2 ACATGTAACAAAGACTTCATTTCGC 28

Db 102 ThrileLysThrArgLeuHisPheGly 110

RESULT 14

```
US-10-127-890-109
; Sequence 109, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-127-890-109
Alignment Scores:
Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 4 Gaps: 0
US-10-717-243-59 (1-28) x US-10-127-890-109 (1-251)
Qy 2 ACATGTAACAAAGACTTCATTGGC 28
Db 102 ThrilelYsthrArgLeuHISpHeGly 110
RESULT 15
; Sequence 110, Application US/10127890
US-10-127-890-109
; Sequence 109, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-127-890-109
Alignment Scores:
Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 4 Gaps: 0
US-10-717-243-59 (1-28) x US-10-127-890-109 (1-251)
Qy 2 ACATGTAACAAAGACTTCATTGGC 28
Db 102 ThrilelYsthrArgLeuHISpHeGly 110
RESULT 15
; Sequence 110, Application US/10127890
US-10-127-890-109
; Sequence 109, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-127-890-110
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Pred. No.: 18.5 Length: 251
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 4 Gaps: 0
US-10-717-243-59 (1-28) x US-10-127-890-110 (1-251)
Qy 2 ACATGTAACAAAGACTTCATTGGC 28
Db 102 ThrilelYsthrArgLeuHISpHeGly 110
Search completed: February 17, 2006, 10:11:14
Job time : 108.5 secs
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 17, 2006, 10:07:45 ; Search time 2.2 Seconds

(without alignments)
36.183 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTAACACAGCTTCATTGGC 28

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 107819 segs, 14214640 residues

Total number of hits satisfying chosen parameters: 215638

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs8082p
-USER=US10717243 @CGN 1.1.7 @runat_16022006_160704_2530 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	67.9	13	7	US-11-116-144-68
2	36	67.9	445	7	Sequence 68, Appl
3	35	66.0	472	6	Sequence 11367, A
4	34	64.2	326	7	Sequence 68, Appl
5	34	64.2	326	7	Sequence 382, Appl
6	34	64.2	608	7	Sequence 854, Appl
7	33	62.3	187	6	Sequence 315, Appl
8	33	62.3	522	6	Sequence 65, Appl
9	33	62.3	636	7	Sequence 21, Appl
					Sequence 2449, Ap

c	10	33	62.3	868	7	US-11-098-686-10347	Sequence 10347, A
	11	32	60.4	36	7	US-11-120-308-76	Sequence 76, Appl
	12	32	60.4	127	6	US-10-995-561-605	Sequence 605, App
c	13	32	60.4	211	6	US-10-821-234-1372	Sequence 1372, Ap
c	14	32	60.4	231	7	US-11-132-285-61	Sequence 61, Appl
c	15	32	60.4	238	7	US-11-072-512-3294	Sequence 3294, Ap
	16	32	60.4	273	6	US-10-467-657-6782	Sequence 6782, Ap
	17	32	60.4	319	7	US-11-120-308-80	Sequence 80, Appl
	18	32	60.4	361	7	US-11-120-308-82	Sequence 82, Appl
	19	32	60.4	374	6	US-10-793-626-442	Sequence 442, App
	20	32	60.4	379	7	US-11-052-554A-193	Sequence 193, App
	21	32	60.4	631	6	US-10-813-646-22	Sequence 22, Appl
	22	32	60.4	756	6	US-10-055-877-34	Sequence 34, Appl
	23	32	60.4	756	6	US-10-055-877-187	Sequence 187, App
	24	32	60.4	756	6	US-10-055-877-188	Sequence 188, App
	25	32	60.4	756	6	US-10-055-877-189	Sequence 189, App
	26	32	60.4	830	6	US-10-055-877-32	Sequence 32, Appl
	27	31	58.5	78	7	US-11-031-206-20	Sequence 20, Appl
c	28	31	58.5	93	7	US-11-098-686-11394	Sequence 11394, A
	29	31	58.5	132	7	US-11-031-206-22	Sequence 22, Appl
	30	31	58.5	132	7	US-11-031-206-198	Sequence 198, App
c	31	31	58.5	192	5	US-09-978-360A-576	Sequence 576, App
	32	31	58.5	210	7	US-11-177-509-35	Sequence 35, Appl
	33	31	58.5	210	7	US-11-177-509-36	Sequence 36, Appl
	34	31	58.5	210	7	US-11-177-509-37	Sequence 37, Appl
	35	31	58.5	210	7	US-11-177-509-38	Sequence 38, Appl
	36	31	58.5	210	7	US-11-177-509-39	Sequence 39, Appl
	37	31	58.5	210	7	US-11-177-509-40	Sequence 40, Appl
	38	31	58.5	210	7	US-11-177-509-41	Sequence 41, Appl
	39	31	58.5	210	7	US-11-177-509-42	Sequence 42, Appl
	40	31	58.5	210	7	US-11-177-509-43	Sequence 43, Appl
	41	31	58.5	210	7	US-11-177-509-44	Sequence 44, Appl
	42	31	58.5	210	7	US-11-177-509-45	Sequence 45, Appl
	43	31	58.5	210	7	US-11-177-509-46	Sequence 46, Appl
	44	31	58.5	210	7	US-11-177-509-47	Sequence 47, Appl
	45	31	58.5	210	7	US-11-177-509-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-11-116-144-68
; Sequence 68, Application US/11116144
; Publication No. US2005027181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LILOP
; APPLICANT: OLLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: INL-084
; CURRENT APPLICATION NUMBER: US/11/116.144
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 68
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-116-144-68
Alignment Scores:
Pred. No.: 7.64 Length: 13
Score: 36.00 Matches: 6
Percent Similarity: 75.0% Conservative: 0
Best Local Similarity: 75.0% Mismatches: 2
Query Match: 67.9% Indels: 0

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DB: 7 Gaps: 0
US-10-717-243-59 (1-28) x US-11-116-144-68 (1-13)
QY 5 TGTAAACAAGACTTCATTGTGGC 28
DB 1 CysLysThrHisProHisPheGly 8

RESULT 2
US-11-098-686-11367
; Sequence 11367, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11367
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11367

Alignment Scores:
Pred. No.: 6.66 Length: 445
Score: 36.00 Matches: 6
Percent Similarity: 85.7% Conservative: 0
Best Local Similarity: 85.7% Mismatches: 1
Query Match: 67.9% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-098-686-11367 (1-445)
QY 22 ATGAAGTCTGTTTACATGT 2
DB 316 MetGlySerCysPheThrCys 322

RESULT 3
US-10-689-742-68
; Sequence 68, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaValle, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-68

Alignment Scores:
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Pred. No.: 10.7 Length: 472
Score: 35.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 66.0% Indels: 0
DB: 6 Gaps: 0

US-10-717-243-59 (1-28) x US-10-689-742-68 (1-472)
QY 25 AAAATGAAGTCTGTTTACA 5
DB 129 LysileLysSerCysPheThr 135

RESULT 4
US-11-000-463-382
; Sequence 382, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-382

Alignment Scores:
Pred. No.: 17.6 Length: 326
Score: 34.00 Matches: 5
Percent Similarity: 77.8% Conservative: 2
Best Local Similarity: 55.6% Mismatches: 2
Query Match: 64.2% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-000-463-382 (1-326)
QY 1 CACATGTAACAAAGACTTCATTGTG 27
DB 264 HisLeuHisasnLysThrGlyTrpTrp 272

RESULT 5
US-11-000-463-854
; Sequence 854, Application US/11000463
; Publication No. US20050266423A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 854
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-854

Alignment Scores:
Pred. No.: 17.6 Length: 326
Score: 34.00 Matches: 5
Percent Similarity: 77.8% Conservative: 2
Best Local Similarity: 55.6% Mismatches: 2
Query Match: 64.2% Indels: 0
DB: 7 Gaps: 0

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QY 1 CACATGTAACAAAGACTTCATTGG 27
Db 264 HsLeuHisAsnLysThrGlyTrpTrp 272

RESULT 6
; Sequence 315, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 315
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-315

Alignment Scores:
Pred. No.: 17.2 Length: 608
Score: 34.00 Matches: 6
Percent Similarity: 66.7% Conservative: 0
Best Local Similarity: 66.7% Mismatches: 3
Query Match: 64.2% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-024-959-315 (1-608)
QY 28 GCCAAATGAAGTCTTGTTTACATGT 2
Db 337 AlAlysGlyLysGlyCysPheLysCys 345

RESULT 7
US-10-980-388-65
; Sequence 65, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiesbsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App.
; FILE REFERENCE: 00325.US1.
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-65

Alignment Scores:
Pred. No.: 29 Length: 187
Score: 33.00 Matches: 5
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 62.3% Indels: 0
DB: 6 Gaps: 0

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US-10-717-243-59 (1-28) x US-10-980-388-65 (1-187)

OY 16 TCTTGTTCATCATGT 2
Db 129 SerCysPheThrCys 133

RESULT 8

US-10-519-390-21
; Sequence 21, Application US/10519390
; Publication No. US2006000872A1
; GENERAL INFORMATION:
; APPLICANT: MEDEXGEN Inc.
; APPLICANT: CHUNG, Yong-Hoon
; APPLICANT: LEE, Hak-sup
; APPLICANT: YI, Ki-Wan
; APPLICANT: KIM, Jae-Youn
; APPLICANT: HEO, Youn-Hwa

; TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/519,390

; CURRENT FILING DATE: 2004-12-23

; PRIOR APPLICATION NUMBER: KR10-2003-0051846

; PRIOR FILING DATE: 2003-07-26

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: Kopatentin 1.71

; SEQ ID NO 21

; LENGTH: 522

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: M-CSF: 35th, 37th, 54th, 67th, 91st, 106th, 121st, 135th, 143rd,
; OTHER INFORMATION: 229th, 255th, 311st, 439th, 466th or 485th Phe is replaced by

US-10-519-390-21

Alignment Scores:

Pred. No.:	27.9	Length:	522
Score:	33.00	Matches:	5
Percent Similarity:	100.0%	Conservative:	2
Best Local Similarity:	71.4%	Mismatches:	0
Query Match:	62.3%	Indels:	0
DB:	6	Gaps:	0

US-10-717-243-59 (1-28) x US-10-519-390-21 (1-522)

OY 25 AAAATGAAGTCTGTGTTTACA 5

Db 86 ArgLeuLysSerCysPheThr 92

RESULT 9

US-11-072-512-2449
; Sequence 2449, Application US/11072512
; Publication No. US20060029945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO

; APPLICANT: SEKI, NAOHIKO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOKYU

; APPLICANT: NAGAHARI, KENJI

; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2449
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2449

Alignment Scores:

Pred. No.:	27.6	Length:	636
Score:	33.00	Matches:	6
Percent Similarity:	66.7%	Conservative:	0
Best Local Similarity:	66.7%	Mismatches:	3
Query Match:	62.3%	Indels:	0
DB:	7	Gaps:	0

US-10-717-243-59 (1-28) x US-11-072-512-2449 (1-636)

OY 2 ACATGTAAACAAGACTTCATTTGGC 28

Db 234 ThrCysHisArgArgLeuHisThrGly 242

RESULT 10

US-11-098-686-10347

; Sequence 10347, Application US/11098686

; Publication No. US20060024696A1

; GENERAL INFORMATION:

; APPLICANT: Kapur, Vivek and Gebhart, Connie J.

; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

; FILE REFERENCE: 09531-128001

; CURRENT APPLICATION NUMBER: US/11/098,686

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: PCT/US03/31318

; PRIOR FILING DATE: 2003-10-01

; PRIOR APPLICATION NUMBER: US 60/416,395

; PRIOR FILING DATE: 2002-10-04

; NUMBER OF SEQ ID NOS: 11433

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10347

; LENGTH: 868

; TYPE: PRT

; ORGANISM: Lawsonia intracellularis

US-11-098-686-10347

Alignment Scores:

Pred. No.:	27.3	Length:	868
Score:	33.00	Matches:	5
Percent Similarity:	100.0%	Conservative:	2
Best Local Similarity:	71.4%	Mismatches:	0
Query Match:	62.3%	Indels:	0
DB:	7	Gaps:	0

US-10-717-243-59 (1-28) x US-11-098-686-10347 (1-868)

OY 25 AAAATGAAGTCTGTGTTTACA 5

Db 624 ArgMetArgSerCysPheThr 630

RESULT 11

US-11-120-308-76

; Sequence 76, Application US/11120308

; Publication No. US20060005277A1

; GENERAL INFORMATION:

APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 76
LENGTH: 36
TYPE: PRT
ORGANISM: Zea mays
US-11-120-308-76

Alignment Scores:
Pred. No.: 49.9 Length: 36
Score: 32.00 Matches: 5
Percent Similarity: 75.0% Conservative: 1
Best Local Similarity: 62.5% Mismatches: 2
Query Match: 60.4% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-120-308-76 (1-36)

QY 5 TGTAAACAGACTTCATTTGCG 28
DB 7 CysAsnThrArgIleLeuPheGly 14

RESULT 12
Sequence 605, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 605
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-605

Alignment Scores:
Pred. No.: 47.5 Length: 127
Score: 32.00 Matches: 4
Percent Similarity: 87.5% Conservative: 3
Best Local Similarity: 50.0% Mismatches: 1
Query Match: 60.4% Indels: 0

DB: 6 Gaps: 0
US-10-717-243-59 (1-28) x US-10-995-561-605 (1-127)
QY 5 TGTAAACAGACTTCATTTGCG 28
DB 78 CysArgSerSerValHisPheGly 85

RESULT 13
US-10-821-234-1372
Sequence 1372, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1372
LENGTH: 211
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1372

Alignment Scores:
Pred. No.: 46.6 Length: 211
Score: 32.00 Matches: 5
Percent Similarity: 83.3% Conservative: 0
Best Local Similarity: 83.3% Mismatches: 1
Query Match: 60.4% Indels: 0
DB: 6 Gaps: 0

US-10-717-243-59 (1-28) x US-10-821-234-1372 (1-211)

QY 19 AAGTCTTCTTTTACATGT 2
DB 50 LysSerCysPheLeuCys 55

RESULT 14
US-11-132-285-61
Sequence 61, Application US/11132285
Publication No. US20050244876A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
FILE REFERENCE: PFS11PI
CURRENT APPLICATION NUMBER: US/11/132,285
CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: US/10/046,433
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/261,960
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/618,570
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/144,087
PRIOR APPLICATION NUMBER: 60/149,450
PRIOR APPLICATION NUMBER: 60/149,450
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: 60/149,712
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/153,089
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 231

Job time : 12 secs

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-61

Alignment Scores:
Pred. No.: 46.4 Length: 231
Score: 32.00 Matches: 5
Percent Similarity: 75.0% Conservative: 1
Best Local Similarity: 62.5% Mismatches: 2
Query Match: 60.4% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-132-285-61 (1-231)

Qy 25 AAAATGAAGTCTGTGTTTACATGT 2
Db 57 LysCysGlnSerCysIleThrCys 64

RESULT 15
US-11-072-512-3294
; Sequence 3294, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3294
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3294

Alignment Scores:
Pred. No.: 46.4 Length: 238
Score: 32.00 Matches: 5
Percent Similarity: 83.3% Conservative: 0
Best Local Similarity: 83.3% Mismatches: 1
Query Match: 60.4% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-072-512-3294 (1-238)

Qy 19 AAGTCTGTTTACATGT 2
Db 128 LysSerCysPheCysCys 133

Search completed: February 17, 2006, 10:11:42
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 17, 2006, 09:46:44 ; Search time 4.8 seconds

(without alignments)
112.253 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTAACACAGACTTCATTGTC 28

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+np.model -DEV=xlp
-Q=/abes/ABSWEB/spool/US10717243/runat_16022006_160652_2247/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=opt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USERS=US10717243 @CN_1_63 @runat_16022006_160652_2247 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	81.1	316	2 JT0753	rRNA N-glycosidase
2	40	75.5	133	2 S69759	hypothetical prote
3	37	69.8	391	2 T32156	hypothetical prote
4	37	69.8	1024	2 T4415	probable leucine p
5	37	69.8	1226	2 E84923	hypothetical prote
6	36	67.9	117	2 PH1542	Ig H chain V regio
7	36	67.9	117	2 PH1552	Ig H chain V regio
8	36	67.9	381	2 T47144	hypothetical prote
9	35	66.0	107	2 T48759	hypothetical prote
10	35	66.0	108	2 H69834	hypothetical prote
11	35	66.0	245	2 C70090	hypothetical prote
12	35	66.0	379	2 A35878	class I major hist
13	35	66.0	406	2 B35878	class I major hist
14	35	66.0	516	2 A48678	activin receptor I

15	35	66.0	570	2 T37407	hypothetical prote
16	35	66.0	2278	1 S56274	FAB1 protein - yea
17	34.5	65.1	186	2 T44425	hypothetical prote
18	34	64.2	104	2 E69767	transcription regu
19	34	64.2	161	2 F86223	protein T12M4.18 [
20	34	64.2	239	2 T17778	hypothetical prote
21	34	64.2	256	2 AD3163	hypothetical prote
22	34	64.2	280	2 G01884	LIM protein PHU-1,
23	34	64.2	280	2 G02741	skeletal muscle LI
24	34	64.2	304	2 F98864	hypothetical prote
25	34	64.2	315	2 T50561	SIN1 protein [imp
26	34	64.2	368	2 T26971	hypothetical prote
27	34	64.2	445	2 C56604	thymidine kinase (
28	34	64.2	489	2 S15349	mdm2 protein - mou
29	34	64.2	501	2 T36466	hypothetical prote
30	34	64.2	601	2 B75136	hypothetical prote
31	34	64.2	693	2 C87575	sensor histidine k
32	34	64.2	772	2 S69577	hypothetical prote
33	34	64.2	1008	2 T05578	hypothetical prote
34	34	64.2	1017	2 S67804	LRG1 protein - yea
35	34	64.2	1077	2 T41146	probable cysteine-
36	34	64.2	1364	2 T14900	condensin XCAP-D2
37	33	62.3	55	2 G82524	hypothetical prote
38	33	62.3	62	2 S73154	hypothetical prote
39	33	62.3	77	1 MNIH3	nonstructural prot
40	33	62.3	129	2 T22430	hypothetical prote
41	33	62.3	152	2 D87282	recombination prot
42	33	62.3	195	2 T02338	senescence-associa
43	33	62.3	200	2 T42678	hypothetical prote
44	33	62.3	216	2 S61701	hypothetical prote
45	33	62.3	237	1 S11927	licheninase (BC 3.

ALIGNMENTS

RESULT 1

JT0753 rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum

N:Alternate names: gelonin; type I ribosome-inactivating protein

C:Species: Gelonium multiflorum

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C:Accession: JT0753; S16489

R:Nolan, P.A.; Garrison, D.A.; Better, M.

Gene 134, 223-227, 1993

A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating pro

A:Reference number: JT0753; PMID:94085781; PMID:7916721

A:Accession: JT0753

A:Molecule type: mRNA

A:Residues: 1-316 <NOL>

A:Cross-references: UNIPROT:P33186; UNIPARC:UPI0000133948; GB:L12243; NID:G388633; PIDN

R:Montecucci, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Soria, M.; Lappi, D.

Int. J. Pept. Protein Res. 33, 263-267, 1989

A:Title: N-terminal sequence of some ribosome-inactivating proteins.

A:Reference number: S16331; PMID:89326691; PMID:2753596

A:Accession: S16489

A:Molecule type: protein

A:Residues: 47-89, K',91-92, 'D' <MON>

A:Cross-references: UNIPARC:UPI0000177F26

C:Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase

F1-46/Domain: signal sequence #status predicted <SIG>

F47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>

F53-294/Domain: rRNA N-glycosidase homology <RNG>

Alignment Scores:

Pred. No.: 1.37 Length: 316
Score: 43.00 Matches: 8
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 1
Query Match: 81.1% Indels: 0
DB: 2 Gaps: 0

C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1542
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A>Title: Molecular characterization of the humoral responses to *Cryptococcus neoformans*
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1542
A:Molecule type: mRNA
A:Residues: 1-117 <MUK>
A:Cross-references: UNIPARC:UPI000017698C
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 43.7 Length: 117
Score: 36.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 67.9% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x PH1542 (1-117)
QY 5 TGTAAACAGACTTCATTTCGC 28
Db 95 CysLysThrArgArgTyPheGly 102

RESULT 7
PH1552
Ig H chain V region (clone 16E4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: PH1552
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A>Title: Molecular characterization of the humoral responses to *Cryptococcus neoformans*
A:Reference number: PH1528; MUID:93210465; PMID:8459205
A:Accession: PH1552
A:Molecule type: mRNA
A:Residues: 1-117 <MUK>
A:Cross-references: UNIPARC:UPI000017695E
A>Note: the stop codon X appears in residue 87
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 43.7 Length: 117
Score: 36.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 67.9% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x PH1552 (1-117)
QY 5 TGTAAACAGACTTCATTTCGC 28
Db 95 CysLysThrArgArgTyPheGly 102

RESULT 8
T47144
Hypothetical protein DKFZP761E1347.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47144
R:Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24374
A:Accession: T47144
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-381 <AA>
A:Cross-references: UNIPARC:UPI000016ACD1; EMBL:AL161962
A:Experimental source: adult amygdala; clone DKFZP761E1347
C:Genetics:
A>Note: DKFZP761E1347.1

Alignment Scores:
Pred. No.: 41 Length: 281
Score: 36.00 Matches: 5
Percent Similarity: 87.5% Conservative: 2
Best Local Similarity: 62.5% Mismatches: 1
Query Match: 67.9% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x T47144 (1-381)
QY 25 AAAATGAAGTCTTGTTCATGT 2
Db 154 LysLeuLysTyrCysTyThrCys 161

RESULT 9
T48759
Hypothetical protein 13E11.70 [imported] - *Neurospora crassa*
C:Species: *Neurospora crassa*
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C:Accession: T48759
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24541
A:Accession: T48759
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <SCH>
A:Cross-references: UNIPARC:UPI000017947A; EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.70
A:Experimental source: cosmid contig 13E11; strain 74
C:Genetics:
A:Gene: NCSP:13E11.70
A:Map position: 2
C:Superfamily: *Neurospora crassa* hypothetical protein 13E11.70

Alignment Scores:
Pred. No.: 71.5 Length: 107
Score: 35.00 Matches: 6
Percent Similarity: 85.7% Conservative: 0
Best Local Similarity: 85.7% Mismatches: 1
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x T48759 (1-107)
QY 5 TGTAAACAGACTTCATTTT 25
Db 77 CysLysThrLeuLeuHisPhe 83

RESULT 10
H6934
Hypothetical protein yhjQ - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H6934
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chac, A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F. Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel, y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seroi, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: H69834
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <KUN>
A:Cross-references: UNIPROT:O07571; UNIPARC:UPI00000601B7; GB:Z99109; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yhjQ

Alignment Scores:
Pred. No.: 71.5 Length: 108
Score: 35.00 Matches: 5
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 83.3% Mismatches: 0
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x H69834 (1-108)

Qy 19 AAGTCTGTGTTTACATGT 2
Db 94 LysAlaCysPheThrCys 99
||||:|||||

RESULT 11

C70090
hypothetical protein yycO - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C70090
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Enian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex
lechi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C70090
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-245 <KUN>
A:Cross-references: UNIPROT:Q45607; UNIPARC:UPI0000060CF9; GB:Z99124; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yycO

Alignment Scores:
Pred. No.: 68.3 Length: 245
Score: 35.00 Matches: 7
Percent Similarity: 87.5% Conservative: 0
Best Local Similarity: 87.5% Mismatches: 1
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x C70090 (1-245)

Qy 3 CATGTAAACAGACTTCATTGT 26
Db 61 HisValLysGlnAspValIleLeu 68
|||||

RESULT 12

A35878
class I major histocompatibility antigen PCC3-4/27 - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
A:Reference number: A35878
R:Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A:Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: A35878
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ITO>
A:Cross-references: UNIPROT:Q31615; UNIPARC:UPI0000028B40; GB:M35243; NID:9199647; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 66.7 Length: 379
Score: 35.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x A35878 (1-379)

Qy 25 AAAATGAAGTCTGTTTACATGT 2
Db 356 LysIleLysSerCysLysThrCys 363
||||:|||||

RESULT 13

B35878
class I major histocompatibility antigen PCC3-24 - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
C:Accession: B35878
R:Ito, K.; Van Kaer, L.; Bonneville, M.; Hsu, S.; Murphy, D.B.; Tonegawa, S.
Cell 62, 549-561, 1990
A:Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam
A:Reference number: A35878; MUID:90335964; PMID:2379238
A:Accession: B35878
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-406 <ITO>
A:Cross-references: UNIPROT:Q31206; UNIPARC:UPI0000028342; GB:M35244; NID:9199663; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 66.4 Length: 406
Score: 35.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x B35878 (1-406)

Qy 25 AAAATGAAGTCTGTTTACATGT 2
Db 356 LysIleLysSerCysLysThrCys 363
||||:|||||

RESULT 14

A48678
activin receptor II precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Dec-2004
C:Accession: A48678
R:Childs, S.R.; Wrana, J.L.; Arora, K.; Attisano, L.; O'Connor, M.B.; Massague, J.
Proc. Natl. Acad. Sci. U.S.A. 90, 9475-9479, 1993
A:Title: Identification of a *Drosophila* activin receptor.
A:Reference number: A48678; MUID:94022397; PMID:8415726

A:Accession: A48678
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-516 <CHI>
A:Cross-references: UNIPROT:Q24229; UNIPARC:UPI0000075D2; GB:L22176; NTD:G408504; PIDN:

C:Genetics:
A:Gene: FlyBase:put
A:Cross-references: FlyBase:FBgn0003169
C:Keywords: ATP
F:200-494/Domain: protein kinase homology <KIN>

Alignment Scores:
Pred. No.: 65.6 Length: 516
Score: 35.00 Matches: 6
Percent Similarity: 85.7% Conservative: 0
Best Local Similarity: 85.7% Mismatches: 1
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x A48678 (1-516)

QY 25 AAATGAAGTCTTTTACA 5

DB 83 LysMetLysGlyCysPheThr 89

RESULT 15

T27407

hypothetical protein: Y7588A.25 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004

C:Accession: T27407

R:Barlow, K.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z20361

A:Accession: T27407

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-570 <WIL>

A:Cross-references: UNIPROT:Q9XW62; UNIPARC:UPI00000767FB; EMBL:AL033514; PIDN:CAA22109

A:Experimental source: clone Y7588A

C:Genetics:

A:Gene: CESP:Y7588A.25

A:Introns: 38/2; 128/2; 327/3; 389/3; 475/1; 518/3

Alignment Scores:

Pred. No.: 65.2 Length: 570
Score: 35.00 Matches: 6
Percent Similarity: 85.7% Conservative: 0
Best Local Similarity: 85.7% Mismatches: 1
Query Match: 66.0% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x T27407 (1-570)

QY 2 ACATGTAAACAAAGACTTCAT 22

DB 519 ThrCysLysProArgLeuHis 525

Search completed: February 17, 2006, 09:52:22

Job time : 26 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 17, 2006, 09:42:19 ; Search time 29.5 Seconds

(without alignments)
133.931 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTAACCAAGACTTCATTGGC 28

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p.model -DEV=xlp
-Q=/abs/ABSSWEB_spool/US0717243/runat_16022006_160650_2211/app_query.fasta_1
-DB=UniProt -QFWT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US0717243 @CN_1_1_466 @runat_16022006_160650_2211 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	45	84.9	283	Q68023 ARATH	Q68023 arabidopsis
C 2	45	84.9	365	Q680U6 ARATH	Q680U6 arabidopsis
C 3	45	84.9	382	Q67X87 ARATH	Q67X87 arabidopsis
C 4	45	84.9	383	Q58FY4 ARATH	Q58FY4 arabidopsis
C 5	45	84.9	383	Q8GUT1 ARATH	Q8GUT1 arabidopsis
C 6	43	81.1	316	R1FG_GELMU	P3186 gelonium mu
C 7	43	81.1	465	Q890L7 CLOTE	Q890L7 clostridium
C 8	39	73.6	109	Q5JS06 HUMAN	Q5JS06 homo sapien
C 9	39	73.6	253	Q5YST2 MOUSE	Q5YST2 mus musculus
C 10	39	73.6	258	Q9S9E4_GELMU	Q9S9E4 gelonium mu
C 11	39	73.6	303	Q5JYH0_HUMAN	Q5JYH0 homo sapien
C 12	39	73.6	305	Q7FQ26_ANOGA	Q7FQ26 anopheles g
C 13	39	73.6	329	Q4SGG7_TETNG	Q4SGG7 tetraodon n
C 14	39	73.6	371	Q5JS05 HUMAN	Q5JS05 homo sapien
C 15	39	73.6	384	Q8CFN0_MOUSE	Q8CFN0 mus musculus
C 16	39	73.6	388	1 ZDH18_HUMAN	Q9NUE0 homo sapien

C 17	39	73.6	388	2 Q7ZVN4 BRARE	Q7ZVN4 brachydanio
C 18	39	73.6	409	2 Q4RLK6_TETNG	Q4RLK6 tetraodon n
C 19	39	73.6	410	2 Q6NLJ6_DROME	Q6NLJ6 drosophila
C 20	39	73.6	481	2 Q8BNR2_MOUSE	Q8BNR2 mus musculus
C 21	39	73.6	488	1 ZDH14_HUMAN	Q81ZN3 homo sapien
C 22	39	73.6	488	2 Q5JS07_HUMAN	Q5JS07 homo sapien
C 23	39	73.6	489	2 Q8BQQ1_MOUSE	Q8BQQ1 mus musculus
C 24	39	73.6	513	2 Q5SNY0_BRARE	Q5SNY0 brachydanio
C 25	39	73.6	750	2 Q3VTW6_DROME	Q3VTW6 drosophila
C 26	39	73.6	862	2 Q4SH44_TETNG	Q4SH44 tetraodon n
C 27	38	71.7	236	2 Q589R6_CIOIN	Q589R6 ciona intes
C 28	38	71.7	251	2 Q5BLG9_BRARE	Q5BLG9 brachydanio
C 29	38	71.7	349	2 Q6KAC3_ORYSA	Q6KAC3 oryza sativ
C 30	38	71.7	397	2 Q4H2K8_CIOIN	Q4H2K8 ciona intes
C 31	38	71.7	457	2 Q55A36_DICDI	Q55A36 dictyosteli
C 32	38	71.7	610	2 Q4PHN5_USTMA	Q4PHN5 uscilago ma
C 33	38	71.7	1048	2 Q86KY8_DICDI	Q86KY8 dictyosteli
C 34	38	71.7	1146	2 Q55A34_DICDI	Q55A34 dictyosteli
C 35	38	71.7	1203	2 Q86KZ0_DICDI	Q86KZ0 dictyosteli
C 36	38	71.7	1216	2 Q8BUP1_MOUSE	Q8BUP1 m mus muscu
C 37	38	71.7	1886	2 Q8XKE5_9VIRU	Q8XKE5 petunia vei
C 38	38	71.7	2179	2 Q91DM0_9VIRU	Q91DM0 petunia vei
C 39	38	71.7	2180	2 Q6XKE6_9VIRU	Q6XKE6 petunia vei
C 40	37	69.8	111	2 Q82RR3_STRAW	Q82RR3 streptomyce
C 41	37	69.8	118	2 Q13629_HUMAN	Q13629 homo sapien
C 42	37	69.8	150	2 Q61RE2_CAEBR	Q61RE2 caenorhabdi
C 43	37	69.8	151	2 Q67ZG8_ARATH	Q67ZG8 arabidopsis
C 44	37	69.8	151	2 Q9LRY6_ARATH	Q9LRY6 arabidopsis
C 45	37	69.8	159	2 Q6NMD4_ARATH	Q6NMD4 arabidopsis

ALIGNMENTS

RESULT 1

Q68023 ARATH

ID Q68023 ARATH PRELIMINARY; PRT; 283 AA.

AC Q68023; 25-OCT-2004 (Tremblrel. 28, Created)

DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)

DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)

DE Hypothetical protein At2g40640.

GN Name=At2g40640;

OS Arabidopsis thaliana (Mouse-ear cress);

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi

OX NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,

RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,

RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,

RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,

RA Hayashizaki Y., Shinozaki K.;

RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) CDNAs.";

RL Submitted (SEP-2004) to the EMBL/GenBank/DDSB databases.

DR EMBL; AK15724; BAD3487.1; -; mRNA.

KW EMBL; AK157678; BAD3441.1; -; mRNA.

KW Hypothetical protein.

SQ SEQUENCE 283 AA; 31924 MW; 51EEF916B14D92DE CRC64;

Alignment Scores:

Pred. No.: 2.04 Length: 283

Score: 45.00 Matches: 7

Percent Similarity: 100.0% Conservative: 1

Best Local Similarity: 87.5% Mismatches: 0

Query Match: 84.9% Indels: 0

DB: Gaps: 0

US-10-717-243-59 (1-28) x Q68023_ARATH (1-283)

QY 25 AAAATGAAGTCTTGTGTTTACATGT 2

|||||||:|||||||

Alignment

RA Xiao Y., Smith S.R., Ishmael N., Kumar N., Redman J., Riedmuller S.,
 RA Utterback T., Whitelaw C.A., Fraser C.M., Town C.D.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY168999; AAC11670.1; -; mRNA.
 RW Hypothetical protein.
 SQ SEQUENCE 383 AA; 43206 MW; 9993C935E4BF1C99 CRC64;

Alignment Scores:
 Pred. No.: 2.1 Length: 383
 Score: 45.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 87.5% Mismatches: 0
 Query Match: 84.9% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q8GUT1_ARATH (1-383)
 QY 25 AAAATGAAGTCTGTGTTTACATGT 2
 |||||:::|||||||
 Db 237 LysMetLysAlaCysPheThrCys 244

RESULT 6
 RIPG_GELMU STANDARD; PRT; 316 AA.
 AC P33186;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-
 DE glycosidase).
 GN Name=GEL;
 OS Gelonium multiflorum (Euphorbiaceae himalayal).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 OC Gelonieae; Gelonium.
 OC NCBI_TaxID=3979;
 RN [1]_TaxID=3979;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;
 RA Nolan P.A., Garrison D.A., Better M.;
 RT "Cloning and expression of a gene encoding gelonin, a ribosome-
 RT inactivating protein from Gelonium multiflorum."
 RL Gene 134:223-227(1993).
 RN [2]
 RP PROTEIN SEQUENCE OF 47-93.
 RC TISSUE=Seed;
 RX MEDLINE=89326691; PubMed=2753596;
 RA Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
 RA Lappi D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins."
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=95333189; PubMed=7608981;
 RA Hoer M.V., Nair B., Satyamurthy P., Misquith S., Surolia A.,
 RA Kannan K.K.;
 RT "X-ray structure of gelonin at 1.8-A resolution."
 RL J. Mol. Biol. 250:368-380(1995).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L12243; AAA16312.1; -; mRNA.
 DR PIR; JT0753; JT0753.

DR HSSP; P09989; 1MRJ.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 KW PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
 KW Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 26
 FT PROPEP 27 46
 FT CHAIN 47 297
 FT PROPEP 298 316
 FT ACT_SITE 212 212
 FT CARBOHYD 235 235
 FT DISULFID 90 96
 FT CONFLICT 90 90
 FT CONFLICT 93 93
 FT CONFLICT 93 93
 SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;
 Alignment Scores:
 Pred. No.: 5.66 Length: 316
 Score: 43.00 Matches: 8
 Percent Similarity: 88.9% Conservative: 0
 Best Local Similarity: 88.9% Mismatches: 1
 Query Match: 81.1% Indels: 0
 DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x RIPG_GELMU (1-316)
 QY 2 ACATGTAACAAGACTTCATTGTCG 28
 |||||:::|||||||
 Db 148 ThrIleLysThrArgLeuHisPheGly 156

RESULT 7
 Q890L7_CLOTE PRELIMINARY; PRT; 465 AA.
 AC Q890L7;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE DNA repair protein rada.
 OS Name=rada; OrderedLocustNames=CTC02630;
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1513;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Massachusetts / B88;
 RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
 RA Brueggemann H., Baumer S., Fricke W.F., Wierzer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 RT tetanus disease."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:13116-1321(2003).
 DR EMBL; AE015945; AAC07080.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004176; F:ATP-dependent peptidase activity; IEA.
 DR GO; GO:0003684; F:damaged DNA binding; IEA.
 DR GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006310; F:DNA recombination; IEA.
 DR GO; GO:0006281; F:DNA repair; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001984; Peptidase_S16.
 DR InterPro; IPR004504; Rada.
 DR PRINTS; PR001553; RECA.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMs; TIGR00416; sms; 1.

DR PROSITE; PS50162; RECA_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 465 AA; 51817 MW; 1472774706CD2B7B CRC64;

Alignment Scores:
 Pred. No.: 5,86 Length: 465
 Score: 43.00 Matches: 7
 Percent Similarity: 88.9% Conservative: 1
 Best Local Similarity: 77.8% Mismatches: 1
 Query Match: 91.1% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q890L7_CLOTE (1-465)

Qy 28 GCCAAATGAAGTCTGTTTACATGT 2
 |||||:|||||
 Db 13 AlalysilleLysSerCysPheValCys 21

RESULT 8
 Q5JS06 HUMAN
 ID Q5JS06 HUMAN PRELIMINARY; PRT; 109 AA.
 AC Q5JS06;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Zinc finger, DHHC domain containing 14 (fragment).
 GS ORFNames=RP3-481C9.1-003;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Johnson C.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Almeida J.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL450328; CAI39700.1; -; Genomic_DNA.
 DR EMBL; AL133510; CAI42854.1; -; Genomic_DNA.
 DR EMBL; AL133510; CAI39700.1; JOINED; Genomic_DNA.
 DR EMBL; AL450328; CAI42854.1; JOINED; Genomic_DNA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR InterPro; IPR001594; Znf_DHHC.
 DR Pfam; PF01529; ZF-DHHC; 1.
 DR PROSITE; PS50216; ZF_DHHC; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 12147 MW; 415F90439F4866DF CRC64;

Alignment Scores:
 Pred. No.: 38.6 Length: 109
 Score: 39.00 Matches: 6
 Percent Similarity: 87.5% Conservative: 1
 Best Local Similarity: 75.0% Mismatches: 1
 Query Match: 73.6% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q5JS06_HUMAN (1-109)

Qy 25 AAAATGAAGTCTGTTTACATGT 2
 |||||:|||||
 Db 20 LysLeulysTyrCysPheThrCys 27

RESULT 9
 Q5Y5T2 MOUSE
 ID Q5Y5T2 MOUSE PRELIMINARY; PRT; 253 AA.
 AC Q5Y5T2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE DHHC-containing protein 18.
 GN Name=Zdhc18;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Fukata M., Fukata Y., Bredt D.S.;
 RT "DHHC-containing proteins";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY668950; AAU89704.1; -; mRNA.
 DR MGI; MGI:3527792; Zdhc18.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF01529; zf-DHHC; 1.
 DR PRODOM; PD003041; Znf_DHHC; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS50216; ZF_DHHC; 1.
 SQ SEQUENCE 253 AA; 27743 MW; 7FA252BA7E4A17E8 CRC64;

Alignment Scores:
 Pred. No.: 41.7 Length: 253
 Score: 39.00 Matches: 6
 Percent Similarity: 87.5% Conservative: 1
 Best Local Similarity: 75.0% Mismatches: 1
 Query Match: 73.6% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q5Y5T2_MOUSE (1-253)

Qy 25 AAAATGAAGTCTGTTTACATGT 2
 |||||:|||||
 Db 55 LysLeulysTyrCysPheThrCys 62

RESULT 10
 Q5S9E4 GELMU
 ID Q5S9E4 GELMU PRELIMINARY; PRT; 258 AA.
 AC Q5S9E4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE rRNA - glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Gelonium multiflorum (Euphorbiaceae himalaya).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 OC Geloniaceae; Gelonium.
 OX NCBI_TaxID=3979;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96006751; PubMed=7553224;
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
 Toman P.D., Cheung L.;
 RT "Amino acid sequence analysis, gene construction, cloning, and
 expression of gelonin, a toxin derived from Gelonium multiflorum.";
 RL J. Interferon Cytokine Res. 15:547-555 (1995).
 DR HSSP; P09989; ILMRJ.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Alignment Scores:
 Pred. No.: 41.7 Length: 258
 Score: 39.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 73.6% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q9S9E4_GELMU (1-258)
 QY 8 AAAACAAGACTTCATTTGGC 28
 DB 111 LysThrArgLeuHisPheGly 117

RESULT 11
 Q5JYHO HUMAN
 ID Q5JYHO_HUMAN PRELIMINARY; PRT; 303 AA.
 AC Q5JYHO;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Zinc finger, DHHC domain containing 18.
 GN Name=ZDHHC18; ORFNames=RP1-50024.3-001;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RA Whitehead S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL034380; CAI21624.1; -; Genomic DNA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR InterPro; IPR003006; IG MHC.
 DR ProDom; PD003041; ZnF-DHHC; 1.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 DR PROSITE; PS0216; ZF-DHHC; 1.
 SQ SEQUENCE 303 AA; 33367 MW; C13A27BF2C6C22E5 CRC64;

Alignment Scores:
 Pred. No.: 42.3 Length: 303
 Score: 39.00 Matches: 6
 Percent Similarity: 87.5% Conservative: 1
 Best Local Similarity: 75.0% Mismatches: 1
 Query Match: 73.6% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q5JYHO_HUMAN (1-303)
 QY 25 AAAATGAAGTCTTGTTCATGT 2
 DB 105 LysLeuLeuTy-CysPheThrCys 112

RESULT 12
 Q7PQ26 ANOGA
 ID Q7PQ26_ANOGA PRELIMINARY; PRT; 305 AA.
 AC Q7PQ26;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE ENSANGP000009967 (Fragment).
 GN ORFNames=ENSANGG0000007478;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RA Whitehead S.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL; AAAB01008900; EAA09399.3; -; Genomic DNA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR InterPro; IPR001594; ZnF-DHHC.
 DR Pfam; PF01529; ZF-DHHC; 1.
 DR PROSITE; PS0216; ZF-DHHC; 1.
 FT NON TER 305
 SQ SEQUENCE 305 AA; 34267 MW; 245E6C727CBA3AEA CRC64;

Alignment Scores:
 Pred. No.: 42.4 Length: 305
 Score: 39.00 Matches: 6
 Percent Similarity: 87.5% Conservative: 1
 Best Local Similarity: 75.0% Mismatches: 1
 Query Match: 73.6% Indels: 0
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q7PQ26_ANOGA (1-305)
 QY 1 25 AAAATGAAGTCTTGTTCATGT 2
 DB 134 LysLeuLeuTy-CysPheThrCys 141

RESULT 13
 Q4SGG7 TETNG
 ID Q4SGG7_TETNG PRELIMINARY; PRT; 329 AA.
 AC Q4SGG7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF14594, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00018646001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Croliis H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."
 RN Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

```
CC      preliminary data
DR      EMBL; CAAE01014594; CAG00265.1; -; Genomic_DNA.
FT      NON TER 329
SQ      SEQUENCE 329 AA; 36192 MW; B045DCE5541B538 CRC64;

Alignment Scores:
Pred. No.: 42.7 Length: 329
Score: 39.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 73.6% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q4SGG7_TETNG (1-329)
Qy 25 AAAATGAAGTCTGTTTACATGT 2
Db 124 LysLeuLysTyrCysPheThrCys 131

RESULT 14
Q5JS05_HUMAN
ID Q5JS05_HUMAN PRELIMINARY; PRT; 371 AA.
AC Q5JS05;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Zinc finger, DHHC domain containing 14 (fragment).
GN ORFNames=RP3-481C9.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Johnson C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Almeida J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL450328; CAI39701.1; -; Genomic_DNA.
DR EMBL; AL133510; CAI42855.1; -; Genomic_DNA.
DR EMBL; AL133510; CAI39701.1; JOINED; Genomic_DNA.
DR EMBL; AL450328; CAI42855.1; JOINED; Genomic_DNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR001594; Znf_DHHC.
DR Pfam; PF01529; zf-DHHC; I.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS50216; ZF_DHHC; 1.
FT      NON TER 1
SQ      SEQUENCE 371 AA; 40291 MW; A45CE211B9FE4F4B CRC64;

Alignment Scores:
Pred. No.: 43.1 Length: 371
Score: 39.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 73.6% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q5JS05_HUMAN (1-371)
Qy 25 AAAATGAAGTCTGTTTACATGT 2
Db 46 LysLeuLysTyrCysPheThrCys 53

RESULT 15
Q8CFN0_MOUSE
ID Q8CFN0_MOUSE PRELIMINARY; PRT; 384 AA.
AC Q8CFN0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
```

```
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NEW1 domain containing protein.
GN Name=Zdhhc14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Adipose;
RA Guo J.H.; Chen L.; Yu L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF542387; AAM47141.1; -; mRNA.
DR Ensembl; ENSMUSG0000034265; Mus musculus.
DR MGI; MGI:2653229; Zdhhc14.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR001594; Znf_DHHC.
DR Pfam; PF01529; zf-DHHC; 1.
DR ProDom; PD003041; Znf_DHHC; 1.
DR PROSITE; PS50216; ZF_DHHC; 1.
SQ      SEQUENCE 384 AA; 41836 MW; 5E1BB23A22B22A9B CRC64;

Alignment Scores:
Pred. No.: 43.3 Length: 384
Score: 39.00 Matches: 6
Percent Similarity: 87.5% Conservative: 1
Best Local Similarity: 75.0% Mismatches: 1
Query Match: 73.6% Indels: 0
DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q8CFN0_MOUSE (1-384)
Qy 25 AAAATGAAGTCTGTTTACATGT 2
Db 58 LysLeuLysTyrCysPheThrCys 65
```

Search completed: February 17, 2006, 09:51:29
Job time : 150.5 secs